

Chromosome	Marker	M Bases From ptel	Location of Nearest 98 or 99% identity L1	Gene containing L1	Distance of L1 from Marker (in M bases)
1q	FCGR2A	162.62	98 (167.4)	none	4.78
1q	D1S1679	163.021	98 (167.4)	none	4.34
1q	D1S213	182.58	98 (178.54) 98 (182.4) 98 (182.6)	LOC127055 none none	4.04 0.18 0.02
1q	LAMC1	187.8	99 (185) 98 (186.7) 98 (189.8)	XPR1 None NIBAN	2.8 1.1 0.02
1q	D1S2785	247	99 (244.3) 98 (244.3) 98 (248.7)	RYP2 LOC128172 none	2.7 2.7 1.7
4p	D4S403	28	98 (28) 98 (31)	none none	0 3
4q	D4S2368	168.5	98 (166.2) 99 (169.2)	Similar to testican NEK1	2.3 0.7
6p	D6S2410	53.57	98 (47.72) 99 (48.8)	SUPT3H none	5.58 4.77
16q	D16S415	54.31	98 (54.6)	MGC5149	0.29
	D16S503	65.28	98 (67.7) 99 (70.5)	none none	2.42 5.22

Table 1. Chromosomal location of proposed SLE disease loci and full length high fidelity L1 elements. % sequence identity was determined in comparison to nt 1-884 of accession no. U09116.

Location Marker (M bases from ptel)	Contig	L1 % identity to 1-884 of U09116 location on contig	Gene	Description or mRNA	Additional Description
162.7	NT_004406	91cds 862,690 88,85	LOC127384	XM_060457 Sim to serum amyloid P/crp family	
163.7	NT_026945	88cds 16,919	LOC126821	XM_060193 Dead/deah box helicase	
165.4 D1s1679	NT_004745	97 89cds 2,404,741 88,87,87 87cds 1,349,888	ATF6 DDR2		
167.7	NT_004648	95,90,90,87 88cds 1,489,481	ALDH9A1		
D1S196 Z16503 170.1 (2,830,998)	NT_004668 AL031733 (2,860,000)	98 4,217,155 97,95 95cds 6,071,165 94 94cds 1,194,759 94cds 6,774,236 92 91cds 1,172,510 90 90cds 6,314,453 89cds 9,220,139 88,87,87 86cds 4,403,629 84cds 4,149,207	Near FLJ00024? LOC92233 LOC127890 LOC127910 NME7 LOC127914 NME7 LOC127911 ATF6 LOC127891 LOC127889	Sim to Ewings sarcoma oncogene XM_059191 XM_060726 Nucleoside diphosphate kinase XM_072920 XM_072918 CAMP-dep tran factor XM_059193 XM_072913	

		87cds 2,140,534 86cds 1,510,476 90cds 1,344,710 88cds 469,620 87cds 1,215,001 81cds 994,144 79cds 937,597 84cds 2,231,864	LOC127109 C1ORF9 LOC92346 LOC127091 KIAA1096 LOC127100 LOC127100 LOC127100 LOC127109	XM_002138 XM_044465 XM_043678	
176	NT_021942	81			
176.6	NT_029873	98 4281 97cds 216,844 96,86	Near LOC90354 LOC90354	XM_031117 Sim to Rab6 GTPase act protein	Phosphoty Binding dom
177.6	NT_004470	88			
178.4	NT_029868	98cds 302,955 95cds 46,079 93 92cds 30,009 78cds 479,243	LOC127055 FLJ10416 " LOC127056	XM_060298 Sim to photomorphogenic prot XM_072714	Ribosomal L13e like
179	NT_004398	bit			
112.1	NT_028147	98cds 2,142,361 96cds 563,171 95 94cds 1,036,908 94 93cds 1,520,639 93,92 90cds 1,621,371 90cds 1,596,843 89	LOC132718 LOC132709 FLJ10891 LOC132712 LOC132714 LOC132715 LOC132715	XM_076833 XM_067997 XM_076837 XM_067992 XM_076830	Kruppel-assoc box GNS1_SUR4

		87cds 228,178 86cds 479,677	LCE LOC132707 Sim to Ac- Liketrans el	XM_045523 XM_067995	Long chain fatty Acyl elongase
		84cds 1,928,148 93cds 1,431,709 87cds 1,260,497 87cds 91,217	LOC132717 LOC132714 LOC132713 EGF	XM_076832 XM_067992 XM_067998 XM_003608	Mitogenic; stim phos of H3; LDL rec domain Protect from LDL oxidation
		78cds 1,864,383	LOC132717	XM_076832	
113.9	NT_006371	94cds 574,774 92cds 517,127	CAMK2D LOC133294	 XM_077029-x	Calcium/calmoduli n Dep kinase delta2 May be involved in neuron signaling hippo/ pyramidal cells
114.8	NT_022790	94 87cds 649,533 86	LOC132392	XM_067820	
D4S430 Z17169 115.4 (111,507)	NT_029273 AC053545	92,90,86			
116	NT_028173	94cds 45,911	LOC132747	XM_076846	
116.2	NT_022931	Nss			
116.7	NT_022989	87.88 83cds (17)			
117.4	NT_016599	97			
160.7	NT_023152	98 1,764,039 98 2,130,593 98cds(11 446,551 97,97 94cds 1,473,285	Near LOC133516 LOC133511 LOC133515	XM_077106 XM_068388 Sim pdgf rec like Prot XM_077105	

		94 92cds 1,275,463 92cds 258,166 88,87 87cds 1,399,629 87 82cds 1,884,591 81cds 530,876 80cds 250,195 81cds 1,454,062	LOC133514 ATP10B LOC133515 GLRA1 LOC133512 ATP10B LOC133515	XM_077104 ATPase XM_077105 Glycine rec alpha1 Startle dis/stiff man syndrome XM_077102	Mutated in hyper- Ekplexia (startle dis) – exon 6
163	NT_006788	98 1,682,752 86cds 1,106,028 85cds 377,215 88cds 1,135,192 86cds 370,363	Near LOC134347 SGCD LOC134344 SGCD LOC134344	XM_068801 Sarcoglycan Dystrophin assoc gp XM_056963	Knock out has cardiomyopathy
164.5	NT_029980	Nss			
165.4	NT_007006	85,88,92,81			
166.5	NT_029289	Nss			
167	NT_023255	Nss			
167.3	NT_025716	94			
D5s422 Z16965 (167.97) (380,023) D5S400 D5S410	NT_006983 AC010602 (438,043)	94cds 184,438 91 87cds 349,741 86cds 807,389 82cds 849,502 86cds 619,246 84cds 278,288	LOC134485 LOC134487 LOC134491 LOC134491 LOC134488 LOC134486	Sim to fibulin	Ig domain
172	NT_006907	88,87,87,85			
175.5	NT_023154	96 87cds	LOC133532	XM_077110	

		1,084,950 89cds 596,953 84cds 955,499 75cds 675,271	LOC133527 LOC133530 LOC133527	XM_068392 XM_077109	
0	NT_008060	86,90			
0.7	NT_023779	91			
1.5	NT_023744	97cds(31-463,266	LOC137257	XM_051541 DLGAP2 Concentrated in synaptic junctions; Coprecip with GRIN2A (NMDAR2), APC, and beta-catenin; colocal with DLG4 and GRIN2A in hippo	Interacts with Hom of Drosophila discs tumor supp prot are assoc with NMDA rec and K channel prot; brain and kidney; cand for progressive epilepsy with mental retardation
2.2	NT_008087	94,93 85cds 461,662 81cds (9-448,734	LOC137745 «	XM_070579 Sim to Pto kinase interactor	
3.8	NT_008227	94cds 56,458 86cds 1,825,757 85cds 1,786,802 87cds 1,625,088 94 94cds 1,805,349 84cds 342,566	LOC137940 CSMD1 « « « LOC137946	XM_078497 XM_054838 XM_078501	CUB (found in C1r, C1s, uEGF, and BMP) and sushi multiple domains 1; CCP domain (abundant in complement control proteins)
5.6	NT_023736	88,87			
6.3	NT_023904	Nss			
D8S503 Z23470 7.28 (2,564,262)	NT_019483	98cds 2,224,912 86,86 85cds 2,492,759 92	LOC137062 LOC137065	XM_078189 XM_070213	
10	NT_023868	Nss			
10.2	NT_030035	86			
10.4	NT_026362	85			

10.8	NT_008010	85			
11.2	NT_008175	Nss			
11.6	NT_008128	92			
12.1	NT_008004	90cds 93,373	FDFT1	XM_035680 Cholesterol biosynthesis Rec syndrome	Farnesyl- diphosphate farnesyltransferase 1
12.4	NT_029349	Nss			
13	NT_008161	90cds 1,633,926	LOC137868	XM_059926	Sim to zeta sarcoglycan
13.6	NT_030030	Nss			
21.9	NT_023704	84cds 141,075 86			
22.4	NT_008205	77			
22.9	NT_008300	93cds 319,091			
23.3	NT_008047	Nss			
23.8	NT_023664	Nss			
24.6	NT_008130	95cds 680,765	LOC137815	x	
D8S1771 Z53561 26.48 (517,449)	NT_023666	91,93 91cds 1,277,844 97cds 361,474 86	LOC137104 LOC137097		
27.3	NT_030023	98cds 332,957	BNIP3L	BCL2/adenovirus E1B 19kD- interacting protein 3-like family proapoptotic	Mitochondria; colocalizes with 60 kD hsp-1; proapoptotic fxn; binds BCL2 family members
27.9	NT_008139	99cds 611,028 87,87,86	LOC137822	XM_070621	?
29.5	NT_007988	93			
31	NT_007993	85cds 185,359	WRN RECQL2	Werner syndrome Homolog of RecQ helicase; 3' to 5' exonuclease; Nucleolar; homol gene in C. elegans implicated in silencing of transposons and RNA interference	Scleroderma-like skin changes; subcutaneous calcification; premature arterioscl, DM; acceleration of telomere-driven replicative senescence
101-125	NT_009151				

125	NT_030107	Nss			
129	NT_009215	94cds 1,920,753 88 81cds 2,324,593 99cds(118- 1,215,303	TECTA GRIK4 LOC120493	Tectorin alpha Glutamate rec Sim to LINE RT homolog	deafness XP_062069
D11S934 Z17119 132.8 (1,384,127) D11s925	NT_009115	98 827,840 98 494,488 97cds 3,036,022 94cds 2,758,023 93,93,92,88 83,83,83 84cds 4,978,908 80cds 4,773,040 82cds 880,521 96cds 3,694,083 96cds 3,364,553	Near PIG8 784,102 LOC120253 FEZ1 446,059 Near LOC120251 ITM1 CHEK1 LOC120271 LOC120267 LOC120293 LOC120289 LOC120253 LOC120279 LOC120275	P53-induced gene 8; activates an apoptotic pathway Fasc and elong Protein zeta 1 527,380 550,705 584,640 XM_073548 XM_073545 	Sim to surf gp, Ig fam Axonal outgrowth Sim to etoposide-induced mRNA Integral mem prot checkpoint monitors meiotic recombination
138.3	NT_009056	93cds 1,156,972	LOC120214	XM_07527	
140.3	NT_024213	nss			
141	NT_009276	95,85			
142	NT_024180	bits			
D20S112	NT_011387	99	Near	23,329,380	

Chrom. Location	M Bases From ptel	Contig	%identity to U09116 1-883 Location of L1 in contig	Gene or LocusLink	Description of Gene Or similar Gene	Additional Description
1q	148.2	NT_022052 ?	89			
		NT_004434+	95cds 435,546 94,89 88cds 414,715 82cds 874,365 82cds 867,310	LOC127469 (148.75) as above LOC127475 (149.2) as above	Sim to bM332P19.3 – novel 7 transmembrane receptor rhodopsin family olfactory rec like protein	
		NT_030568	88			
	150	NT_029226-	89cds 737,990	Cezanne (149.8)	Cellular zinc finger anti-NF kappa B – A20-like zinc finger domain (inhib of cell death)	
		NT_004811	Bitcds			
		NT_021907+	89cds 787,136	LOC126632		
		NT_004441	82,87			
		NT_030577 ?	Nss			
	154.5	NT_021933	Nss			
		NT_004524	Nss			
1q22		NT_004858+	85cds 2,260,795 94cds 2,352,293 87cds 2,322,154 84cds 2,355,589 84cds 2,300,855	LOC128249 (157.95) “ “ “ “	Sim to cell surface molecule Ly-9 (CD229) -Ig superfamily (others are CD2, CD48, CD58)	XM_060902 (Ly-9 = AF244129; 29% identical)
		NT_019291-	Bits			
	159	NT_004982+	94cds 1,245,500	LOC128375 (159.83)	Sim to gamma interferon inducible	

			93,88,85,85.84		protein 16	
		NT_030566-	94			
		NT_026222 ?	Nss			
	161	NT_004406-	91cds 862,690 88,85	LOC127384 (160.62)	Sim to porcine Amyloid A protein	Binds to lipid of apoptotic cells
		NT_026945+	88cds 16,919	LOC126821		
D1S1679	163.021	NT_004668				
1003304.121901 105121.102201	162-171	NT_004668-	98(167.4) 4,217,155 97,95	Near FLJ00024? LOC92233 LOC127890	Sim to Ewings sarcoma oncogene XM_059191	Breakpoint region
			-95cds 6,071,165 94	LOC127910	XM_060726	No con dom; drohom
			94cds 1,194,759	NME7 (170.2-.5)	Nucleoside diphosphate kinase	
			-94cds 6,774,236 92	LOC127914 (964.85)	XM_072920	Unfolded prot response FLJ21522 Sim FLJ00024 SH3 dom Phosphoty Interaction Sim transporter
			91cds 1,172,510 90	NME7 (170.5)		
			-90cds 6,314,453	LOC127911	XM)072918	
			-89cds 9,220,139 88,87,87	ATF6 (162.3-.4)	CAMP-dep tran factor; binds SRF	
			-86cds 4,403,629	LOC127891 (167.2)	XM_059193	
			84cds 4,149,207 85	LOC127889	XM_072913	
			-83cds 5,501,845	LOC127906	XM_127906	
			-0cds 1,047,463	LOC57821	NM_021179	
			-87cds 8,510,019 87cds	LOC127934	XM_060744	
					Discoidin domain	Extracell factor

			7,810,544	DDR2 (163.8)	rec fam 2 Neurotrophic tyr kinase rec rel3	VIII-like domain; act by collagen
			88cds 4,815,922 -89cds 3,680,941	ALDH9A1 (166.75) LOC127885	Catal dehydrogen- ation of GABA XM_060709	Sim toFlavin cont Monooxygen5
			-85cds 9,359,548	LOC127944 Near fcfr2b (163.22)	XM_060702 Rib prot L31	
			-85cds 1,467,216	LOC127874	XM_072909	
			-86cds 6,335,176	LOC127911 (165.4)	XM_072918	
			-79cds 6,030,189	LOC127910 (165.5)	XM_060726	
			-3cds ? 6,578,251	LOC127912 (165.05)	XM_060727 Sim to adenyl cyc	
			-86cds ? 6,540,496	LOC127912		
			-81cds 1,040,525	LOC57821	XM_001574	
			81cds 399,716	KIFAP3 (171.08- 171.2)	Kinensin assoc protein 3 Smg GDS-assoc prot SMAP - cerebellum	Armadillo repeats; phos by v-src
D1S196	168.76					
		NT_004732-	87,87,89,87			
		NT_030564-	87cds 201,283	LOC127144 (174.1)		
	175.5	NT_029874+	97cds 286,649	LOC127090 (164.57)	Sim to ganglioside GM2 activator precursor (SAP-2)	Ganglioside gm2 activator precursor protein 3
			96cds 1,900,362	LOC127105	XM_072723	
			95cds 969,927	LOC127100	XM_044463	XP_044463 KIAA0820
			94 93cds 1,227,344	(175.0) LOC127100		Dynamin domain GTPase effector domain (mediate vesicle trafficking);
			89 87cds	LOC127109	XM_060332	

			2,235,511 87cds 2,140,534 86cds 1,510,476 90cds 1,344,710 88cds 469,620 87cds 1,215,001 81cds 994,144 79cds 937,597 84cds 2,231,864	LOC127109 C1ORF9 LOC92346 LOC127091 KIAA1096 LOC127100 LOC127100 LOC127100 (175.6) LOC127109	Sim to rib prot L26 XM_002138 XM_044465 XM_043678	pleckstrin homo
		NT_021942 ?	Bits			
		NT_030570 ?	Nss			
	177.5	NT_004470-	Bits			
		NT_029868+	98cds 302,955 95cds 46,079 93 92cds 30,009 78cds 479,243	LOC127055 (178.54) FLJ10416 (178.3) FLJ10416 LOC127056	Sim to photomorph- Ogenic prot “	
DIS1589 (182.58)		NT_026949+	98 (182.4) 3,396,062 98cds (182.6) 3,597,400 97 97cds 3,809,963 96cds 3,954,485 96 95cds 1,184,773 94 93cds(31 2,588,833 91,90 88cds	? LOC90354 As above LOC126850 LOC126858 LOC126850		

			1,228,754 86,86 83cds 2,432,829 83cds 1,243,379 89cds 3,170,271	FLJ10244 LOC126850 NPHS2 (181.85)	Guanine nuc exchange factor podocin	Like SOS Nephrotic syndrome
	185	NT_004552+	99cds 1,317,693 87 86cds 2,407,307 86cds 2,445,258 79cds 2,487,143 88cds 778,461	XPR1 (184.28) LOC127663 (185.7) as above as above MGC2404 (183.93)	Xenotropic and polytropic retrovirus receptor ???	
		NT_029219+	98 (186.7) 85,973 96,92 96cds 379,853	Near LOC126918 (186.7) LOC126920 (187.15)	Sim to embigin Sim to KIAA0456	
		NT_029880 ?	Nss			
LAMC1 (187.8)	188.6	NT_029864-	93cds 983,033 89,89 78cds 956,095	LOC127028 (188.4) as above		
		NT_004487+	98cds (189.8) 340,228 98 3,128,788 98 2,880,876 95cds 752,376 95,95,93,92 91cds 1,658,122	C1orf24 Near LOC127523 Near LOC127522 And LOC 127521 C1orf26 FIBL-6 (190.65)	Niban Sim to basement membrane specific heparan sulfate PG core protein precursor	

			92cds 879,310 85cds 1,757,301	LOC127514 (190.3) LOC127519	Near PRG4	
		NT_021972-	86cdsbit 272,0623			
	195	NT_021905-	93,91,90			
		NT_004671+	98cds 2,492,213 97 96cds 6924 96	LOC127964 LOC127946	Sim to ribosomal prot L23A -sim to myomegalin	
	200	NT_004599+	84,82			
		NT_021909+	Bits			
		NT_004416-	99 392,676 93cds 551,372	Near LOC127387 (202.65) LOC127388 (202.5)	Sim to H factor 1 – complement Isoform 1 -sim to complement factor H-rel protein 3 precursor – FHR- 3	Also near factor H sushi
		NT_029862+	98 797,582 93 93cds 931,447 88cds 83,139 83cds 255,648 92cds 958,777 96cds 134,515	Near LOC127012 (204.1) LOC127012 FHR5 (203.22) LOC127012 F13B (203.28)	Factor H-rel Prot 5 Coag factor13B	
		NT_030560	88 82cds 258,938	LOC127117		
	207.5	NT_004680+	92,92,89,86			
D1S1678		NT_004662-	93cds 676,800 92cds 481,841 83cds(57 534,300	LOC127827 (212.45) LOC93273 (212.48) LOC127827	Sim to gp330 Sim to thymopoietin	
		NT_021924 ?	88			

	214	NT_029217-	89,88,90		IL-10, DAF area	
		NT_030585+	94,92 87cds 578,468 86cds(757-391,332	LOC127235 (214.92) CR1	Small fragment	
		NT_030579 ?	Nss			
		NT_030575 ?	Nss			
	216	NT_021877+	98cds 1,352.011 92 88cds 1,411.541	LOC126615 (217) as above		
LOC127235		NT_030578-	90cds 1,301,974 89cds 1,294.365 87 87cds 731,351 86 90cds 686,368 88cds 1,381,704 88cds 1,265,982 80cds 1,494,931	KCNH1 (217.84-218.23) KCNH1 MGC14801 (218.52) LOC127190 KCNH1 KCNH1 LOC127192	K voltage-gated channel Sim to p21-Arc	Myoblasts at fusion stage
		NT_004993+	87cds 694,358 87,85 85cds 378,593 87cds 1,417,141	LOC128385 FLJ10874 (219.7) LOC128391		
		NT_029884 ?	Nss			
	222	NT_004612-	93 87cds 1,675,483 89cds 1,674,521 87cds 577,128 87cds	LOC127758 (221.25) as above LOC127742 LOC127758		

			1,593,865			
		NT_030582+	Bits			
1q41	225	NT_004817	98 773,814 96cds 1,098,009 94 88cds 1,364,541 79cds 1,422,107	Near LOC128150 And LOC128149 LOC128153 FLJ10252 (225.25) LOC128155	Glycine rich nucleic acid binding domain	RNA processing protein?
		NT_029863+	Nss			
		NT_029871+	96cds 739,776 93cds 319,420 93cds 295,189	RAB3- GAP150 (228.1) LOC127083 As above	GTPase activating protein	
1q42	229	NT_004642-	86 87cds 146,862 84cds 306,312	LOC127803 LOC127805		
		NT_029866+	86cds 42,308	LOC127046		
		NT_030576 ?	Nss			
	230	NT_021953+	85cds 289,839	LOC126708		
		NT_029858 ?	Nss			
	231	NT_004861+	97 93cds 348,708 93 85cds 179,795 92	LOC128253 FLJ10052 (231.6)	Contains sushi domain ; sim to DAF precursor	
		NT_004525-	83,83,93 83cds 313,463bit	LOC127586 (234.43)	Sim to synapsin I	ADPRTarea (233.45)
	235	NT_004908+	92,87 85cds 42,367	LOC128303		

		NT_004559+	Bits			
	237	NT_021973-	bits			
	238.5	NT_004753-	91cds 543,853	DISC1 (238.61-239.13)	Disrupted in schizophrenia	Multiple sclerosis lesions
D1S3462	238.9	NT_004753	In DISC1			
	240	NT_004433-	96cds(757 10,613	LOC127452		
		NT_030561-	90,88			
		NT_022107 ?	Nss			
D1S235	242.97	NT_004836	In CHS1 243.07			
RYS2= 244.3 244.9 D1S235	244	NT_004836-	99cds 2,329,412 98cds 2,379,197 92,92 88cds 3,235,442 cdspartial	RYS2 (244.3) LOC128172 TM7SF1 (243.38)	Cardiac Increased in kidney transmembrane	Calcium release Channel of sarcoplasmic reticulum
D1S2785	248	NT_004771+	98 (248.7) 1,913,492 92 91cds 771,848	Near LOC114922 RGS7 (147.52)	Sim to pentraxin rel gene-3 GTPase activating	Mostly in brain
	250	NT_004734+	97,87,87 86cds 2,159,228 88cds 870,185	AKT3 (251.3-4) LOC128041 (250.2)	v-akt murine thymoma viral oncogene homolog3	Protein kinase B, gamma; pleckstrin homol domain; Ser/thr kinase
		NT_026947 ?	Nss			
		NT_030586 ?	Bits			
	254	NT_004536+	99 (252.6) 340,220 97 95cds 1,954,493 86 85cds	Near LOC127615 (309,963) And LOC 127616 (354,490) FLJ21080 (254.2) LOC127610	Sim to olf recs SET domain; MYND finger Sim to olf rec	

	.		453,782 85cds 546,320	LOC127622		
	256.4	NT_029870+	97,92,92 94cds 21,328	LOC127057	Sim to olfactory rec 1-25	

Table 3. Contigs on chromosome 1q containing full-length L1 element sequences. Nss signifies no sequence homology to nt 1-884 of accession no. U09116.

for "029870"

M Bases from ptel	Marker	Gene	Contig	L1 element %identical to nt 1-884 of consensus Location in contig
			NT_010552	88
			NT_010540	Nss
			NT_010388	Nss
			NT_027184	Nss
			NT_010543	Nss
			NT_015360	Nss
6.0M			NT_027178	Bit
			NT_010384	Nss
			NT_010537	84
11M		FLJ12668	NT_010530	98 1,112,885 87 87cds 1,997,396
12.5M		FLJ12363	NT_010419	86 92cds 571,065 86,83
		Myosin	NT_010393	86,86,89,89
			NT_024760	Bit
17.3M		LOC115995 Sim to LIP isoform of BLIP	NT_024822	99,3'utr(208- 25,588 91,87
			NT_010584	Nss
20M			NT_024776	Nss
			NT_030153	95
			NT_010436	Nss
			NT_024801	88
			NT_010592	Nss
			NT_027182	88,87
			NT_010604	89,88
27.5M			NT_010591	Nss
			NT_010441	88
			NT_027176	Nss
			NT_010589	Nss
			NT_024802	Nss
32M		ITGAM (CR3 :CD11b)	NT_024812	88cds 447,353

44.3M			NT_028368	89
45M			NT_024773	98 671,001 98 748,545 93,92,92.90.90 88,87
45.5M		PHKB CDA08 CDA08 CDA08 PHKB CDA08 PHKB	NT_010570	96,92, 90cds 564,374 89 84cds 900,968 91 91cds 1,065,272 86cds 810,315 88,85 82cds 700,819 87cds 822,483 85cds 693,085
			NT_010637	Nss
			NT_010505	97,84,87
50M		Near LOC 115613 sim to Na and Cl-dep transpo ZNF267	NT_024779	98 811,937 94,91,88 89cds 596,749
			NT_029461	Nss
			NT_010493	Nss
			NT_010521	86,85,83
54M	D16S 419 D16S415	MGC5149	NT_010498	98cds 746,473 85,96,91
55.8M		AMFR Autocrine motility factor	NT_019610	93,93 89cds 288,196
57.4M			NT_024766	bit
58.6M			NT_010406	94,83
60.2M			NT_029457	95,95,93,86.86
62.5M		CDH8x3 Cadherin 8	NT_010463 CDH8x3	97cds 1,670,319

				96cds 1.689.733 95cds 1.806583 93,93.89
62.9			NT_019621	Nss
63.5			NT_010615	93,92.91
65 (77)	D16S3253 D16S503	0.1/3.2	NT_010558	95,87
66.6			NT_010546	98 758.900 92,92
69.8		Near CDH3 (placental)	NT_010478	99 2.329.912 88
71.1			NT_019608	Nss
71.9			NT_030154	Nss
72.1			NT_028369	bit
72.6		Near DKFZp 434L0850	NT_010635	99 6635
73.1			NT_010580	Nss
73.4			NT_027175	88
74.2			NT_024792	97,86
			NT_029456	Nss
76M		Near LOC93220 Sim to laminin rec 1	NT_010556	99 782.847
			NT_030151	Nss
			NT_024793	84
78M			NT_010480	85
			NT_030152	Nss
			NT_024797	Bits
			NT_026456	Nss
			NT_024827	87.86
			NT_024821	Nss
			NT_010380	93
			NT_010422	97,86,80
			NT_028372	Nss
			NT_010494	Bits
			NT_024814	96,94,90,84
86.5M		CDH13 (heart)	NT_010428	99cds 701.822
			NT_028371	Nss

Table 4. Location of full-length L1 elements on chromosome 16. Nss signifies no significant homology with nt 1-884 of L1 consensus sequence in accession no. U09116.

Location M Bases from ptel	Contig or BAC clone	L1 element %identity to consensus 1- 884 location in contig	Gene
7.8M	NT_029490	80	
APP AD1 11-39.6M 23.9M	NT_011512	97 22,448,995 97 1,963,309 97 20,880,812 97cds 12,869,179 96,94,93 93cds 26,987,787 93,91 90cds 24,057,658 89,89,88 87cds 27,064,029 86,86,85	APP DSCAM TTC3 DSCAM
11M	AP001464	Nss	
	AJ239321	89	
	AP001170	Nss	
	AP001135	Nss	
	AJ239318	Nss	
	AL049911	Nss	
	AL050302	Nss	
	AL078475	Nss	
	AP001465	Nss	
	AL163204	86	
	AL109748	Nss	
	AP001466	Nss	
	AP001634	83	
	AP001347	89	
	AL078615	Nss	
	AF130358	83	
	AF130249	Nss	STCH
	AF130247	Nss	
12.6	AF165138	Nss	
	AF198098	88	

	AF130351	Nss	
	AF127936	88	
	AF248484	97 86,680 87	
	AF127577	97 9772 87	
	AF222684	Nss	
	AF222685	Nss	
13.3	AF130248	Nss	
	AF246928	Nss	
	AJ006998	Nss	
	AJ009632	Nss	
	AJ006997	Nss	
	AL034449	Nss	
	AJ010597	Nss	
	AJ010598	91	
14	AL109762	91	
	AP001344	Nss	
	AP001346	89	
	AP001343	80	
	AP001172	Nss	
	AP000962	Nss	
14.65	AP000473	Nss	
	AF130359	76	
	AF212831	Nss	
	AF130418	93,90	
	AP001250	Nss	
	AP000457	85,93,85,86	
	AP000968	94	
	AP000952	96	
	AP000963	Nss	
15.6	AP000967	Nss	
	AP000432	Nss	
	AL109761	80	
	AP000404	Nss	
	AP000745	Nss	
	AF165175	Nss	
16	AP000998	Nss	
	AF130417	Nss	
	AP000656	Nss	
	AL078474	Nss	
	AP000456	Nss	
16.45	AP000455	Nss	

	AL109763	Nss	
	AF240627	Nss	
	AP001538	93	
17	AL157359	Nss	
	AP001345	Nss	
	AP000431	Nss	
	AP000433	Nss	
	AP000855	Nss	
	AP000958	Nss	
	AP000566	83	
	AP000401	Nss	
	AP000403	Nss	
	AP000568	Nss	
	AP000946	Nss	
17.9	AF238375	Nss	
	AP001256	Nss	
	AP001171	Nss	
18.3	AP001254	Nss	D21S1437
	AP001251	Nss	
18.6	AP001506	Nss	
	AL109772	Nss	
	AP000957	Nss	
	AP000947	Nss	
	AL035532	Nss	
	AP000460	83	
19	AF135405	Nss	
	AP001138	Nss	
	AP001136	Nss	
	AP001252	Nss	
	AP001137	Nss	
	AP001114	Nss	
	AP001115	Nss	
	AP001117	Nss	
	AF241725	Nss	
	AP000475	Nss	
	AP000472	Nss	
	AP000454	Nss	
20.05	AP000951	Nss	
	AP000705	82	
	AP000657	Nss	
	AP000561	Nss	
	AP000953	Nss	
	AP000959	82	
	AP000966	Nss	
	AP000955	Nss	

20.9	AP000949	Nss	
	AP001116	Nss	
	AP001255	Nss	
	AP001253	Nss	
	AP000459	Nss	
	AP000965	Nss	
	AP000950	Nss	
	AP000961	Nss	
	AP000960	Nss	
	AP000474	Nss	
	AP000477	Nss	
22.1	AP000470	Nss	
	AP000469	Nss	
	AP000458	Nss	
	AP000954	Nss	
	AP000476	Bit	
	AP001079	Nss	
	AP000964	Nss	
	AP000948	Nss	
	AP000402	Nss	
	AP000146	Bit	
	AP001342	Nss	
	AP000235	Nss	
	AP000234	Nss	
	AP000233	Nss	
	AP000232	Nss	
	AP001341	Nss	
	AP001340	Nss	
	AP001348	Nss	
	AP000220	Bits	
	AP000221	Nss	
	AL109616	Nss	
	AP000223	Nss	
	AP000224	Nss	
	AP000225	Nss	
	AP000226	Nss	
	AP000227	Nss	
	AP000228	Nss	
	AP001443	Nss	APP
23.9M	AP001442	97cds 7857	APP
	AP001440	Nss	APP
	AP001441	Nss	APP
	AP001439	bit	APP

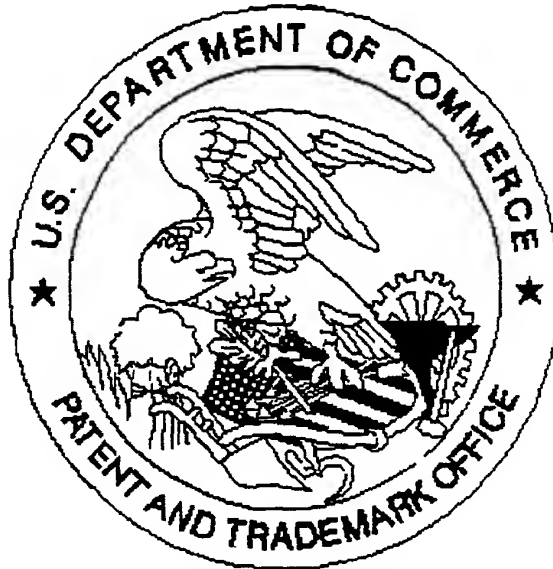
	AP000229	Nss	
	AP000230	Nss	
	AP001595	Nss	
	AP001596	Nss	

33.9	AF020802	Nss	
	AP000687	Nss	
	AP000688	Nss	
	AP000689	Nss	
	AP000690	Nss	
	AP000691	Nss	
	AP000692	80	
	AP000693	Nss	
	AP000694	Nss	
	AP000695	Nss	
	AP000696	86	
34.6	AP000697	Nss	
	AP000698	Nss	
	AP000699	Nss	
	AP000700	Nss	
	AP000701	Nss	
	AP000702	Nss	
	AP000703	Nss	
	AP001418	Nss	
	AP000704	Nss	
	AP001435	Nss	
	AP001431	Nss	
	AP001429	90	TTC3
35.1	AP001432	Nss	TTC3 DSCR3
	AP001412	Nss	DSCR3
	AP001437	Nss	
	AP001428	Nss	
	AP001413	Nss	
	AP001421	Nss	
	AP001414	Nss	
	AP001419	Nss	
	AP001407	Nss	
	AP001436	Nss	
35.7	AP001416	Nss	
	AP001430	Nss	
	AP001408	Nss	
	AP001411	Nss	
	AP001424	Nss	
	AP001433	Nss	

39.5	AP001610	nss	
39.6M	---	Nss	
	NT_030187		
40.5	NT_030188	Bit	
43	NT_011515	bit	

Table 5. Location of full-length L1 elements on chromosome 21. Nss signifies no significant homology with nt 1-884 of L1 consensus sequence in accession no. U09116

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